

OIPE

## RAW SEQUENCE LISTING

DATE: 06/21/2001

PATENT APPLICATION: US/09/875,321

TIME: 17:19:21

Input Set : A:\10448-061001.TXT

Output Set: N:\CRF3\06212001\I875321.raw

ENTERED

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4 <110> APPLICANT: Curtis, Rory A.J.
6 <120> TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM
7   CHANNEL FAMILY MEMBERS AND USES THEREOF
10 <130> FILE REFERENCE: 10448-061001
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/875,321
C--> 12 <141> CURRENT FILING DATE: 2001-06-06
12 <150> PRIOR APPLICATION NUMBER: US 60/209,845
13 <151> PRIOR FILING DATE: 2000-06-06
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3525
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (638)...(3178)
28 <400> SEQUENCE: 1
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30 tcccgcagcg gccaaaggcag ggctcaggcc ccgggattct cccacacgc tgctgcactg      120
31 gcgcagccgg tcgcaaaact ttttctcccc aaagccagtg ccccgagcagt tacttggcgg      180
32 gcagccggca gccactctc ggccgggatga tctgggagaa gcgggcgtgg gacgagggg      240
33 ctgctgtttt gcagccctgc gaggcgtgca gtcggagaag tggtcggggg tccacaccgt      300
34 ccttgagcct gccccctggc caaggtggcc gcacgtgctg cagtggctgg cgcaggtgat      360
35 ccgggcagcg gctccggcac tagtcaagg ggacgcggca cgggaggag gggcgcttt      420
36 ctcttttctc ctccccctgc agcccagctg cactgcgtgg gggctctcca tctccacgca      480
37 atcagcaggc ggaatccctg ccctggagcg ccctggctct ggactgcacc cccctagggg      540
38 ttgtcctgca gattctctc cccatctttc tctgccacac acgttccct aagccgcgcg      600
39 cgccgcaaac tcagtctcgg tcccgcagg tgatgtc atg ccc att gtt ttg gtg      655
40                                     Met Pro Ile Val Leu Val
41                                     1           5
43 cgc cca acc aat cgg act cgc cgc ctg gat tct acc gga gcc ggc atg      703
44 Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp Ser Thr Gly Ala Gly Met
45           10           15           20
47 ggc cct tcc tcg cac cag cag cag gag tcc ccg ctc ccg acc ata acg      751
48 Gly Pro Ser Ser His Gln Gln Gln Glu Ser Pro Leu Pro Thr Ile Thr
49           25           30           35
51 cat tgc gca ggg tgc acc acc gct tgg tct ccc tgc agc ttt aac agc      799
52 His Cys Ala Gly Cys Thr Thr Ala Trp Ser Pro Cys Ser Phe Asn Ser
53           40           45           50
55 cct gac atg gaa acc cca ttg cag ttc cag cgc ggc ttc ttc cca gag      847
56 Pro Asp Met Glu Thr Pro Leu Gln Phe Gln Arg Gly Phe Phe Pro Glu
57 55           60           65           70
59 cag ccg ccg ccg ccg ccg cgc tcc tca cac ctg cat tgc cag cag cag      895
60 Gln Pro Pro Pro Pro Pro Arg Ser Ser His Leu His Cys Gln Gln Gln
61           75           80           85
63 caa cag agc cag gac aag ccg tgc ccg ccc ttc gcg ccc ctc ccg cac      943

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64	Gln	Gln	Ser	Gln	Asp	Lys	Pro	Cys	Pro	Pro	Phe	Ala	Pro	Leu	Pro	His	
65				90					95					100			
67	cct	cac	cac	cac	ccg	cac	ctc	gcg	cac	cag	cag	ccg	gcc	agc	ggc	ggc	991
68	Pro	His	His	His	Pro	His	Leu	Ala	His	Gln	Gln	Pro	Ala	Ser	Gly	Gly	
69			105					110					115				
71	agc	agc	cca	tgc	ctc	cgg	tgc	aac	agc	tgc	gcc	tcc	tcc	ggt	gcc	ccg	1039
72	Ser	Ser	Pro	Cys	Leu	Arg	Cys	Asn	Ser	Cys	Ala	Ser	Ser	Gly	Ala	Pro	
73		120					125					130					
75	gcg	gcg	ggg	gcg	gga	gat	aac	ctg	tcc	ctg	ctg	ctc	cgc	acc	tcc	tcg	1087
76	Ala	Ala	Gly	Ala	Gly	Asp	Asn	Leu	Ser	Leu	Leu	Leu	Arg	Thr	Ser	Ser	
77	135					140				145						150	
79	ccc	ggc	ggc	gcc	ttc	cgg	acc	cgc	acc	tcc	tcg	ccg	ctg	tcg	ggc	tcg	1135
80	Pro	Gly	Gly	Ala	Phe	Arg	Thr	Arg	Thr	Ser	Ser	Pro	Leu	Ser	Gly	Ser	
81				155						160					165		
83	tcc	tgc	tgc	tgc	tgc	tgc	tgc	tcg	tcg	cgc	cgg	ggc	agc	cag	ctc	aat	1183
84	Ser	Cys	Cys	Cys	Cys	Cys	Cys	Ser	Ser	Arg	Arg	Gly	Ser	Gln	Leu	Asn	
85			170					175					180				
87	gtg	agc	gag	ctg	acg	ccg	tcc	agc	cat	gcc	agt	gcg	ctc	cgg	cag	cag	1231
88	Val	Ser	Glu	Leu	Thr	Pro	Ser	Ser	His	Ala	Ser	Ala	Leu	Arg	Gln	Gln	
89			185				190						195				
91	tac	gcg	cag	cag	tcc	gcg	cag	cag	tcg	gcg	tcc	gcc	tcc	cag	tac	cac	1279
92	Tyr	Ala	Gln	Gln	Ser	Ala	Gln	Gln	Ser	Ala	Ser	Ala	Ser	Gln	Tyr	His	
93		200				205						210					
95	cag	tgc	cac	agc	ctg	cag	ccc	gcc	gcc	agc	ccc	acg	ggc	agc	ctc	ggc	1327
96	Gln	Cys	His	Ser	Leu	Gln	Pro	Ala	Ala	Ser	Pro	Thr	Gly	Ser	Leu	Gly	
97	215				220					225					230		
99	agt	ctg	ggc	tcc	ggg	ccc	ccg	ctc	tcg	cac	cac	cac	cac	cac	ccg	cac	1375
100	Ser	Leu	Gly	Ser	Gly	Pro	Pro	Leu	Ser	His	His	His	His	His	Pro	His	
101				235						240					245		
103	ccg	gcg	cac	cac	cag	cac	cac	cag	ccc	cag	gcg	cgc	cgc	gag	agc	aac	1423
104	Pro	Ala	His	His	Gln	His	His	Gln	Pro	Gln	Ala	Arg	Arg	Glu	Ser	Asn	
105			250					255					260				
107	ccc	ttc	acc	gaa	ata	gcc	atg	agc	agc	tgc	agg	tac	aac	ggg	ggc	gtc	1471
108	Pro	Phe	Thr	Glu	Ile	Ala	Met	Ser	Ser	Cys	Arg	Tyr	Asn	Gly	Gly	Val	
109			265				270					275					
111	atg	cgg	ccg	ctc	agc	aac	ttg	agc	gcg	tcc	cgc	cgg	aac	ctg	cac	gag	1519
112	Met	Arg	Pro	Leu	Ser	Asn	Leu	Ser	Ala	Ser	Arg	Arg	Asn	Leu	His	Glu	
113		280				285						290					
115	atg	gac	tca	gag	gcg	cag	ccc	ctg	cag	ccc	ccc	gcg	tct	gtc	gga	gga	1567
116	Met	Asp	Ser	Glu	Ala	Gln	Pro	Leu	Gln	Pro	Pro	Ala	Ser	Val	Gly	Gly	
117	295				300					305					310		
119	ggt	ggc	ggc	gcg	tcc	tcc	ccg	tct	gca	gcc	gct	gcc	gcc	gcc	gcc	gct	1615
120	Gly	Gly	Gly	Ala	Ser	Ser	Pro	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
121				315						320					325		
123	gtt	tcg	tcc	tca	gcc	ccc	gag	atc	gtg	gtg	tct	aag	ccc	gag	cac	aac	1663
124	Val	Ser	Ser	Ser	Ala	Pro	Glu	Ile	Val	Val	Ser	Lys	Pro	Glu	His	Asn	
125			330					335					340				
127	aac	tcc	aac	aac	ctg	gcg	ctc	tat	gga	acc	ggc	ggc	gga	ggc	agc	act	1711
128	Asn	Ser	Asn	Asn	Leu	Ala	Leu	Tyr	Gly	Thr	Gly	Gly	Gly	Gly	Ser	Thr	

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129	345	350	355	
131	gga gga ggc ggc ggc ggt ggc ggg agc ggg cac ggc agc agc agt ggc	1759		
132	Gly Gly Gly Gly Gly Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly			
133	360 365 370			
135	acc aag tcc agc aaa aag aaa aac cag aac atc ggc tac aag ctg ggc	1807		
136	Thr Lys Ser Ser Lys Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly			
137	375 380 385 390			
139	cac cgg cgc gcc ctg ttc gaa aag cgc aag cgg ctc agc gac tac gcg	1855		
140	His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala			
141	395 400 405			
143	ctc atc ttc ggc atg ttc ggc atc gtg gtc atg gtc atc gag acc gag	1903		
144	Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu			
145	410 415 420			
147	ctg tcg tgg ggc gcc tac gac aag gcg tcg ctg tat tcc tta gct ctg	1951		
148	Leu Ser Trp Gly Ala Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu			
149	425 430 435			
151	aaa tgc ctt atc agt ctc tcc acg atc atc ctg ctc ggt ctg atc atc	1999		
152	Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile			
153	440 445 450			
155	gtg tac cac gcc agg gaa ata cag ttg ttc atg gtg gac aat gga gca	2047		
156	Val Tyr His Ala Arg Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala			
157	455 460 465 470			
159	gat gac tgg aga ata gcc atg act tat gag cgt att ttc ttc atc tgc	2095		
160	Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys			
161	475 480 485			
163	ttg gaa ata ctg gtg tgt gct att cat ccc ata cct ggg aat tat aca	2143		
164	Leu Glu Ile Leu Val Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr			
165	490 495 500			
167	ttc aca tgg acg gcc cgg ctt gcc ttc tcc tat gcc cca tcc aca acc	2191		
168	Phe Thr Trp Thr Ala Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr			
169	505 510 515			
171	acc gct gat gtg gat att att tta tct ata cca atg ttc tta aga ctc	2239		
172	Thr Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu			
173	520 525 530			
175	tat ctg att gcc aga gtc atg ctt tta cat agc aaa ctt ttc act gat	2287		
176	Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp			
177	535 540 545 550			
179	acc tcc tct aga agc att gga gca ctt aat aag ata aac ttc aat aca	2335		
180	Thr Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr			
181	555 560 565			
183	cgt ttt gtt atg aag act tta atg act ata tgc cca gga act gta ctc	2383		
184	Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu			
185	570 575 580			
187	ttg gtt ttt agt atc tca tta tgg ata att gcc gca tgg act gtc cga	2431		
188	Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg			
189	585 590 595			
191	gct tgt gaa agg tac cat gat caa cag gat gtt act agc aac ttc ctt	2479		
192	Ala Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu			
193	600 605 610			

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195 gga gcg atg tgg ttg ata tca ata act ttt ctc tcc att ggt tat ggt      2527
196 Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly
197 615                      620                      625                      630
199 gac atg gta cct aac aca tac tgt gga aaa gga gtc tgc tta ctt act      2575
200 Asp Met Val Pro Asn Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr
201                      635                      640                      645
203 gga att atg ggt gct ggt tgc aca gcc ctg gtg gta gct gta gtg gca      2623
204 Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala
205                      650                      655                      660
207 agg aag cta gaa ctt acc aaa gca gaa aaa cac gtg cac aat ttc atg      2671
208 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met
209                      665                      670                      675
211 atg gat act cag ctg act aaa aga gta aaa aat gca gct gcc aat gta      2719
212 Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn Ala Ala Asn Val
213                      680                      685                      690
215 ctc agg gaa aca tgg cta att tac aaa aat aca aag cta gtg aaa aag      2767
216 Leu Arg Glu Thr Trp Leu Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys
217 695                      700                      705                      710
219 ata gat cat gca aaa gta aga aaa cat caa cga aaa ttc ctg caa gct      2815
220 Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala
221                      715                      720                      725
223 att cat caa tta aga agt gta aaa atg gag cag agg aaa ctg aat gac      2863
224 Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Asn Asp
225                      730                      735                      740
227 caa gca aac act ttg gtg gac ttg gca aag acc cag aac atc atg tat      2911
228 Gln Ala Asn Thr Leu Val Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr
229                      745                      750                      755
231 gat atg att tct gac tta aac gaa agg agt gaa gac ttc gag aag agg      2959
232 Asp Met Ile Ser Asp Leu Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg
233                      760                      765                      770
235 att gtt acc ctg gaa aca aaa cta gag act ttg att ggt agc atc cac      3007
236 Ile Val Thr Leu Glu Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His
237 775                      780                      785                      790
239 gcc ctc cct ggg ctc ata agc cag acc atc agg cag cag cag aga gat      3055
240 Ala Leu Pro Gly Leu Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp
241                      795                      800                      805
243 ttc att gag gct cag atg gag agc tac gac aag cac gtc act tac aat      3103
244 Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp Lys His Val Thr Tyr Asn
245                      810                      815                      820
247 gct gag cgg tcc cgg tcc tcc agg agg cgg cgg tcc tct tcc aca      3151
248 Ala Glu Arg Ser Arg Ser Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr
249                      825                      830                      835
251 gca cca cca act tca tca gag agt agc tagaagagaa taagttaacc      3198
252 Ala Pro Pro Thr Ser Ser Glu Ser Ser
253                      840                      845
255 acaaaataag actttttgcc atcatatggt caatatattta gctttttattg taaagcccct      3258
256 atggtttctaa tcagcgttat ccgggttctg atgtcagaat cctgggaacc tgaacactaa      3318
257 gtttttaggcc aaaatgagtg aaaactcttt ttttttcttt cagatgcaca gggaatgcac      3378
258 ctattattgc tatatagatt gttcctcctg taattttcact aactttttat tcatgcactt      3438

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259 caaacaaaact ttactactac attatatgat atataataaa aaaagttaat ttctgcaaaa 3498
260 aaaaaaaaaa aaaaaaaaaac ggacggg 3525
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 847
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 2
268 Met Pro Ile Val Leu Val Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp
269 1 5 10 15
270 Ser Thr Gly Ala Gly Met Gly Pro Ser Ser His Gln Gln Gln Glu Ser
271 20 25 30
272 Pro Leu Pro Thr Ile Thr His Cys Ala Gly Cys Thr Thr Ala Trp Ser
273 35 40 45
274 Pro Cys Ser Phe Asn Ser Pro Asp Met Glu Thr Pro Leu Gln Phe Gln
275 50 55 60
276 Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Arg Ser Ser His
277 65 70 75 80
278 Leu His Cys Gln Gln Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro
279 85 90 95
280 Phe Ala Pro Leu Pro His Pro His His His Pro His Leu Ala His Gln
281 100 105 110
282 Gln Pro Ala Ser Gly Gly Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys
283 115 120 125
284 Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu
285 130 135 140
286 Leu Leu Arg Thr Ser Ser Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser
287 145 150 155 160
288 Ser Pro Leu Ser Gly Ser Ser Cys Cys Cys Cys Cys Cys Ser Ser Arg
289 165 170 175
290 Arg Gly Ser Gln Leu Asn Val Ser Glu Leu Thr Pro Ser Ser His Ala
291 180 185 190
292 Ser Ala Leu Arg Gln Gln Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala
293 195 200 205
294 Ser Ala Ser Gln Tyr His Gln Cys His Ser Leu Gln Pro Ala Ala Ser
295 210 215 220
296 Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His
297 225 230 235 240
298 His His His His Pro His Pro Ala His His Gln His His Gln Pro Gln
299 245 250 255
300 Ala Arg Arg Glu Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys
301 260 265 270
302 Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn Leu Ser Ala Ser
303 275 280 285
304 Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln Pro Leu Gln Pro
305 290 295 300
306 Pro Ala Ser Val Gly Gly Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala
307 305 310 315 320
308 Ala Ala Ala Ala Ala Val Ser Ser Ser Ala Pro Glu Ile Val Val
309 325 330 335

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date